using modern techniques such as multi-spacer typing or DNA microarray.

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31.003

The Use of Genomics for the Early Diagnosis of Scrub Typhus and Other Systemic Infectious Diseases

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Genomic tools and approaches have enabled a more detailed description of host-microbe encounters, and shed light on fundamentally important processes, including the cellular responses associated with infection. Genome-wide transcript-abundance profiles, like other comprehensive molecular readouts of host physiological state, provide a detailed blueprint of the host-pathogen dialogue during microbial disease. Studies of cancer based on genome-wide transcript-abundance profiles have led to novel signatures that predict disease outcome and serve as useful clinical classifiers. The highly dynamic and compartmentalized aspects of the host response to pathogens complicates efforts to identify predictive signatures for infectious diseases. Yet, studies of systemic infectious diseases so far suggest the possibility of successfully discriminating between different types (classes) of infection and predicting clinical outcome. We have collected and analyzed genome-wide transcript abundance patterns early in the course of nonspecific acute febrile illness, and found evidence for classification on the basis of microbial diagnosis. Scrub typhus appeared to have a distinct signature in one study, but this finding needs to be validated. Early explorations in host genomic response profiling suggest the possibility of recognizing etiological factor(s) and predicting the course of disease, at early points in the timeline of the process, but also point to important unmet challenges.

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Vector and Epidemiology

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Tsutsugamushi disease (scrub typhus) has a long history of investigation and is still an important disease as re-emerging infectious disease. Geographic distribution of the disease is recognized as the ''Tsutsugamushi triangle'' which extends from Far East Asia, to northern Australia, and to West Asia. The causative agent *Orientia tsutsugamushi* (Ot.) has various serotypes and each has specific vector species of trombiculid mites by endemic areas, and also its pathogenecity is very diverse.

The authors summarize the vectorial competence of main mite species in Asia as follows; From Far Eastern Russia to Korea and mainland Japan, *Leptotrombidium pallidum* is very prevalent both in spring and autumn, and possesses JP (Karp) and JG (Gilliam) type Ot. From East Asia (Korea, China and southern half of Japan) to Southeast Asia, *L. scutellare* makes characteristic distributional pattern as a drastic endemic spot that push up outbreaks in autumn, and is affinitive to Kawasaki, Kuroki and Boryong? type of Ot. From southwestern islands of Japan to Southeast Asia, *L. deliense* is commonly found throughout warm seasons and may transmits various oriental types of Ot. It is interesting that a border dissociating the distributions of *L. scutellare* and *L. deliense* may be in Tokara Islands of southernmost Japan as the Watase line between Palearctic and Oriental regions. Additionally *L. arenicola* and *L. fletcheri* are densely distributed within Southeast Asia, and possesses Ot. types like in *L. deliense*.

Although the clinician must bear in mind that the Tsutsugamushi disease is still an un-neglected disease that causes serious results unless carefully attended, the increasing problems of rickettsioses including Japanese Spotted Fever draw more attention as the infectious diseases.

Investigations concerning the early diagnostic method, treatment and host-pathogen cytokine regulation mechanism are going on.

In those times that humans and things move fast globally, we propose here to establish the International network system on the view of epidemiology of the rickettsial diseases.

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21st Century Global Health Protection (invited)

33.001

21st Century Global Health Protection

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Our 21st century 'flat world' can enable solutions to global health challenges through technologies, communication tools, and economic opportunities that a decade ago were not even imagined. But the flat world is also a world that faces daunting challenges - wars and ideological conflicts, climate change, and extreme poverty - that threaten our progress. Pandemics, terrorist attacks, and extreme weather are among the most likely urgent threats that pose large-scale consequences to human health, economic prosperity, and national security. Solutions to these challenges require not only innovation, but also global health leadership evolution. Successful global leaders will need ''meta-leadership'' skills - the ability to lead horizontally across a complex array of organizations through recognition and development of shared strategic goals, as well as culturally competent methods for adapting and executing these strategies. Ultimately, the entire health network will need to be optimized to assure we have the knowledge and tools to protect people around the globe.

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